AMENDMENTS TO THE CLAIMS

1. – 30. (Canceled)

31. (Currently Amended) A method for producing L-methionine which comprises culturing a recombinant *Escherichia* bacterium in a medium to produce and accumulate L-methionine in the medium in an amount in excess of the corresponding unmodified *Escherichia* bacterium, and collecting the L-methionine from the medium, wherein

the bacterium is deficient in repressor of L-methionine biosynthesis system encoded by the endogenous *metJ* gene and has L-methionine productivity,

activity of intracellular homoserine transsuccinylase encoded by the *metA* gene of a *Escherichia* bacterium is increased compared to an unmodified *Escherichia* bacterium by increasing copy number of the *metA* gene including its own promoter, or replacing the native promoter with a stronger promoter, and

the bacterium comprises at least one characteristic selected from the group consisting of:

(a) exhibits reduced activity of intracellular S-adenosylmethionine synthetase encoded by the endogenous *metK* gene as compared to an unmodified *Escherichia* bacterium;

(b) exhibits L-threonine auxotrophy;

(c) exhibits enhanced activity of intracellular cystathionine γ-synthase encoded by the *metB* gene of a *Escherichia* bacterium and enhanced activity of intracellular aspartokinase-homoserine dehydrogenase II encoded by the *metL* gene of a *Escherichia* bacterium as compared to an unmodified *Escherichia* bacterium by increasing copy number of each of the genes including their own promoters, or replacing the native promoter with a

stronger promoter; and

(d) has a homoserine transsucinylase for which concerted inhibition by L-methionine and S-adenosylmethionine is desensitized, wherein the homoserine transsuccinylase comprising the amino acid sequence of SEQ ID NO: 26 contains at least one amino acid replacement wherein said at least one amino acid replacement is independently selected from the group consisting of replacement of the amino acid residue Arg-27 with cysteine, replacement of the amino acid residue Ile-296 with serine, and replacement of the amino acid residue Pro-298 with leucine.

32. – 34. (Canceled)

35. (Previously Presented) The method according to Claim 31, wherein the bacterium is *Escherichia coli*.

36. – 40. (Canceled)

41. (Previously Presented) The method according to claim 31, wherein the bacterium comprises at least the characteristic (a).

42. (Previously Presented) The method according to claim 31, wherein the bacterium comprises at least the characteristic (b).

43. (Previously Presented) The method according to claim 31, wherein the bacterium comprises at least the characteristic (c).

44. (Previously Presented) The method according to claim 31, wherein the bacterium comprises at least the characteristic (d).

45. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (a) and (b).

46. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (a) and (c).

47. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (a) and (d).

48. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (b) and (c).

49. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (b) and (d).

50. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (c) and (d).

51. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (a), (b), and (c).

52. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (a), (b), and (d).

53. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (a), (c), and (d).

54. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristics (b), (c), and (d).

55. (Previously Presented) The method according to claim 31, wherein the bacterium comprises the characteristic (a), (b), (c), and (d).

56. (Currently Amended) The method according to claim 31, wherein the activity of intracellular S-adenosylmethionine synthetase is reduced due to that the bacterium has S-adenosylmethionine synthetase which contains amino acid substitution which is selected from the group consisting of replacement of the amino acid residue Ile-303 with leucine, replacement of the amino acid residue Val-185 with glutamic acid, and replacement of ~~the amino acid residue Arg-378 and subsequent~~ amino acid residues 378-384 with the amino acid sequence of SEQ ID NO: 29, respectively in the amino acid sequence of SEQ ID NO: 18.

57. (Currently Amended) The method according to claim 41, wherein the activity of intracellular S-adenosylmethionine synthetase is reduced due to that the bacterium has S-adenosylmethionine synthetase which contains amino acid substitution which is selected from the group consisting of replacement of the amino acid residue Ile-303 with leucine, replacement of the amino acid residue Val-185 with glutamic acid, and replacement of ~~the amino acid residue Arg-378 and subsequent~~ amino acid residues 378-384 with the amino acid sequence of SEQ ID NO: 29, respectively in the amino acid sequence of SEQ ID NO: 18.

58. (Previously Presented) The method according to claim 31, wherein the L-threonine auxotrophy is due to deletion of the *thrBC* genes.

59. (Previously Presented) The method according to claim 42, wherein the L-threonine auxotrophy is due to deletion of the *thrBC* genes.